Amendments to the Claims:

Please cancel claims 16-30 without prejudice or disclaimer, as set forth hereafter in the complete listing of the claims.

1. (original) A method for diagnosing a predisposition to fat deposition in a subject, which comprises detecting the presence or absence of a polymorphic variation associated with fat deposition at a polymorphic site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a subject, wherein the PLA2G1B nucleotide sequence comprises a polynucleotide sequence selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:1;

(b) a nucleotide sequence which encodes a polypeptide consisting of the amino acid sequence of SEQ ID NO:2;

(c) a nucleotide sequence which encodes a polypeptide that is 90% identical to the amino acid sequence of SEQ ID NO:2; and

(d) a fragment of a nucleotide sequence of (a), (b), or (c) comprising the polymorphic site;

whereby the presence of the polymorphic variation is indicative of a predisposition to fat deposition in the subject.

2. (original) The method of claim 1, which further comprises obtaining the nucleic acid sample from the subject.

3. (original) The method of claim 1, wherein the polymorphic variation is a guanine at position 7328 of SEQ ID NO:1.

4. (original) The method of claim 3, wherein the polymorphic variation is in linkage disequilibrium with the guanine at position 7328 of SEQ ID NO:1.

5. (original) The method of claim 1, wherein the polymorphic variation is a thymine at position 9182 of SEQ ID NO:1.

6. (original) The method of claim 5, wherein the polymorphic variation is in linkage disequilibrium with the thymine at position 9182 of SEQ ID NO:1.

7. (original) The method of claim 1, wherein detecting the presence or absence of a polymorphic variation comprises:

hybridizing an oligonucleotide to the nucleic acid sample, wherein the oligonucleotide is complementary to the PLA2G1B nucleotide sequence and hybridizes to a region of the PLA2G1B nucleotide sequence that is adjacent to the polymorphic variation;

extending the oligonucleotide in the presence of one or more nucleotides, yielding extension products; and

detecting the presence or absence of the polymorphic variation in the extension products.

8. (previously presented) The method of claim 7, wherein the oligonucleotide is selected from the group consisting of TGAGATGGGAGGATCT (SEQ ID NO: 31), ACTGGGAACCTCGA (SEQ ID NO: 32), GCTGATGCCGCTG (SEQ ID NO: 33), GGAGTGACCCCTT (SEQ ID NO: 34), ACACATGACAACTGCTA (SEQ ID NO: 35), GGTGTGGGTGTACGG (SEQ ID NO: 36), GGTGTGGGTGTACGG (SEQ ID NO: 37), CCACACCTATTCATACTC (SEQ ID NO: 38), CTTAGGCAGGAGAATC (SEQ ID NO: 39), GTAATGCAACTTCAAAC (SEQ ID NO: 40); TTAGCATCCTTCAGGCCTAAA (SEQ ID NO: 57), GACTCTGCCTCAAAATAAATAAAA (SEQ ID NO: 58), GCCGTAGTTGTTGTATTCCAA (SEQ ID NO: 59), GTGCAAAACAGTGGGCGATGCT (SEQ ID NO: 60), TGATTGCCGAGCCAGAGCA (SEQ ID NO: 61), TTTCCATAATAGATATTTATGTAG (SEQ ID NO: 62), ATTAGCTGGGCATGGTGGC (SEQ ID NO: 80), CACTGTACTCTCCAATAAAGCACC (SEQ ID NO: 63), CAAACAAACACACACACAAAAC (SEQ ID NO: 64).

9. (original) The method of claim 1, wherein the fat deposition is central fat deposition in the subject.

10. (original) The method of claim 1, wherein the subject is a human.

11. (original) A method for diagnosing a predisposition to leanness in a subject, which comprises detecting the presence or absence of a polymorphic variation associated with leanness at a polymorphic site in a PLA2G1B nucleotide sequence in a nucleic acid sample from a subject, wherein the PLA2G1B nucleotide sequence is selected from the group consisting of:

(a) the nucleotide sequence of SEQ ID NO:1;

(b) a nucleotide sequence which encodes a polypeptide consisting of the amino acid sequence of SEQ ID NO:2;

(c) a nucleotide sequence which encodes a polypeptide that is 90% identical to the amino acid sequence of SEQ ID NO:2; and

(d) a fragment of a nucleotide sequence of (i), (ii), or (iii) comprising the polymorphic site;

whereby the presence of the polymorphic variation is indicative of leanness in the subject.

12. (original) The method of claim 11, wherein the polymorphic variation is an adenine at position 7328 in SEQ ID NO:1.

13. (original) The method of claim 12, wherein the polymorphic variation is in linkage disequilibrium with the adenine at position 7328 of SEQ ID NO:1.

14. (original) The method of claim 11, wherein the polymorphic variation is a guanine at position 9182 of SEQ ID NO:1.

15. (original) The method of claim 14, wherein the polymorphic variation is in linkage disequilibrium with the guanine at position 9182 of SEQ ID NO:1.

16-30. (cancelled).